

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-10. (cancelled)

11. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising ~~a arbitrary~~ user-specified sequence composition and length, the method comprising:

    a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being intended synthesized to have the a user-specified sequence composition and length and being synthesized by the steps of:

        providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

        providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

        contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

        contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;

    b) distinguishing between error-free and error-containing nucleic acid molecules within said plurality or pool, wherein the error-free nucleic acid molecules are synthesized nucleic molecules that have the user-specified sequence composition and length and the error-containing nucleic acid molecules are synthesized nucleic molecules that do not have the user-specified sequence composition and length; and

Q) selectively amplifying only the error-free nucleic acid molecules from said plurality or pool, thereby decreasing the percentage relative amount of error-containing nucleic acid molecules within said plurality or pool.

12. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising ~~a arbitrary~~ user-specified sequence composition and length, the method comprising:

- a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being intended synthesized to have the a user-specified sequence composition and length and being synthesized by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;

b) distinguishing between error-free and error-containing nucleic acid molecules within said plurality or pool, wherein the error-free nucleic acid molecules are synthesized nucleic molecules that have the user-specified sequence composition and length and the error-containing nucleic acid molecules are synthesized nucleic molecules that do not have the user-specified sequence composition and length; and

c) correcting errors in said plurality or pool by using the error-free nucleic acid molecules in said plurality or pool as a template for repair of said error-containing nucleic acid molecules.

13. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising ~~a arbitrary~~ user-specified sequence composition and length, the method comprising:

- a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being intended synthesized to have the a user-specified sequence composition and length and being synthesized by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;

b) identifying error-containing nucleic acid molecules ~~ones~~ of said nucleic acid molecules, wherein the error-free nucleic acid molecules are synthesized nucleic molecules that have the user-specified sequence composition and length and the error-containing nucleic acid molecules are synthesized nucleic molecules that do not have the user-specified sequence composition and length;

c) removing the error-containing portions of said error-containing nucleic acid molecules to produce error-free nucleic acid sequences; and

d) recombining combining said error-free nucleic acid sequences to yield error-free nucleic acid molecules.

14. (previously amended) The method of claim 11, the step of selectively amplifying further comprising the step of combining at least one error-containing nucleic acid molecule from said

plurality or pool with at least one component that prevents amplification of the error-containing nucleic acid molecule.

15. (currently amended) The method of claim 14, wherein the errors in the error-containing nucleic acid molecule are mismatches and the component is a mismatch binding protein.

16. (previously presented) The method of claim 14, wherein the component is cross-linked to the error-containing nucleic acid molecule.

17. (cancelled)

18. (cancelled)

19. (previously presented) The method of claim 14, wherein the component comprises more than one molecule.

20. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of targeting errors via methylation and selective demethylation.

21. (currently amended) The method of claim 12, wherein the errors in the error-containing nucleic acid molecules are mismatches, the step of correcting errors comprising the steps of:  
mismatch recognition on said error-containing nucleic acid molecules to identify specific base errors in said error-containing nucleic acid molecules;  
cleavage of said specific base errors; and  
replacement of said cleaved base errors with the correct bases according to the template.

22. (previously amended) The method of claim 21, wherein the steps of mismatch recognition and cleavage are performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

23. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by disassociation and reassociation of single-stranded nucleic acid molecules.

24. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by strand invasion.

25. (withdrawn) The method of claim 12, wherein no entire nucleic acid molecules in the plurality or pool need be error-free.

26. (currently amended) The method of claim 13, wherein the errors in the error-containing nucleic acid molecules are mismatches, the step of removing errors comprising the steps of: mismatch recognition on said error-containing nucleic acid molecules to identify specific base sequence errors in said error-containing nucleic acid molecules; and cleavage of said specific base sequence errors.

27. (previously amended) The method of claim 26, wherein the steps of mismatch recognition and cleavage are performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

28. (withdrawn) The method of claim 26, wherein the step of mismatch recognition and cleavage is performed by a single molecule.

29. (currently amended) The method of claim 13, wherein the errors in the error-containing nucleic acid molecules are mismatches and the step of removing errors is performed by a mismatch binding protein to identify specific base sequence errors in said error-containing nucleic acid molecules and a nuclease to cleave said specific base sequence errors.

30. (previously presented) The method of claim 13, wherein no nucleic acid molecules in the plurality or pool need be error-free.